



PI Masure SLJ, Richardson A;  
XX  
XX MPI: 2000-498840/44.  
DR P-PSDB: AAB13393.  
XX  
XX New human serine/threonine kinase protein and the polynucleotide  
PT encoding the protein, useful for preparing a medicament for treating  
PT disorders associated with human serine/threonine kinase protein  
PT activity, especially cancer  
XX  
XX  
PS Claim 3; Fig 1; 61pp; English.  
CC The present sequence encodes human Akt-3. Akt-3 is a third human isoform  
CC of Akt, which is also known as protein kinase B (PKB) or "related to A  
CC and C protein kinase" (RAC-PK). The gene encoding Akt-3 is located on  
CC human chromosome 1, region q43-q44. A human hippocampal EST sequence that  
CC showed high similarity to the rat RAC-PKgamma sequence was used to design  
CC primers for 3' rapid amplification of cDNA ends (3' RACE). The sequence  
CC obtained in the first round of 3' RACE was used to design primers for a  
CC second round. The complete sequence was then amplified from human  
CC hippocampal cDNA by PCR using primers based on the product of the second  
CC round of 3' RACE. Akt can inhibit apoptosis induced by detachment from  
CC the extracellular matrix. The Akt-3 nucleic acid molecule and protein may  
CC be used as medicaments for treating cancer. Agents which influence the  
CC activity of Akt-3 protein, and so stimulate apoptosis, may also be used  
CC to treat diseases associated with Akt-3.  
XX  
SQ Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 other:

Query Match 100.0%; Score 1547; DB 21; Length 1547;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggagtcacatcagcagatgtaccatgttgaaagaagttgggtcagaagaaggagga 60  
DB 1 gggagtcacatcagcagatgtaccatgttgaaagaagttgggtcagaagaaggagga 60  
QY 61 atataataaaactgtgagccaaagatctcctttgaaagacagatggctcattcaag 120  
DB 61 atataataaaactgtgagccaaagatctcctttgaaagacagatggctcattcaag 120  
QY 121 atataagaagaacctcaagatgtgtattacccttaccctcaacaactttcagtgc 180  
DB 121 atataagaagaacctcaagatgtgtattacccttaccctcaacaactttcagtgc 180  
QY 181 aaaaatgcagttatgaataacagaagaccagaacccaacactttatatacagatctc 240  
DB 181 aaaaatgcagttatgaataacagaagaccagaacccaacactttatatacagatctc 240  
QY 241 ccagtcgactactgttatagagaacatttcagttagaactccagaagaaggagaa 300  
DB 241 ccagtcgactactgttatagagaacatttcagttagaactccagaagaaggagaa 300  
QY 301 atggacagaagctatccagctgttagcagacagactcgaaggcagaagaaggagaat 360  
DB 301 atggacagaagctatccagctgttagcagacagactcgaaggcagaagaaggagaat 360  
QY 361 gaattgttaactcaacttcaaatgtatataatagagaaggagaatgtgacctctac 420  
DB 361 gaattgttaactcaacttcaaatgtatataatagagaaggagaatgtgacctctac 420  
QY 421 aaccacatcaataaagaacaatgaatatttgactattgaaactctactaggttaag 480  
DB 421 aaccacatcaataaagaacaatgaatatttgactattgaaactctactaggttaag 480  
QY 481 caactttgggaagtattttgttcgagaagaagcaagtgganaaactactatgttaa 540  
DB 481 caactttgggaagtattttgttcgagaagaagcaagtgganaaactactatgttaa 540  
QY 541 gatttcgagaagaagctatatttgcagaagaatgagcagacactctaaactaaag 600  
DB 541 gatttcgagaagaagctatatttgcagaagaatgagcagacactctaaactaaag 600

QY 601 cagagatataaagaacactagacatcccttttaacatccttgaatatcttccccaagc 660  
DB 601 cagagatataaagaacactagacatcccttttaacatccttgaatatcttccccaagc 660  
QY 661 aaaaagccgtttgtgtttgtatgataatgttaatggggcgaaactgttttccactt 720  
DB 661 aaaaagccgtttgtgtttgtatgataatgttaatggggcgaaactgttttccactt 720  
QY 721 gtccagaagcggtgttctctgtgagaccgacacagttctatgtgtcagaatgtctc 780  
DB 721 gtccagaagcggtgttctctgtgagaccgacacagttctatgtgtcagaatgtctc 780  
QY 781 tgccttgagctatcactatccgaaagatgtgtacccgtgtacatcctaagtgtgagaact 840  
DB 781 tgccttgagctatcactatccgaaagatgtgtacccgtgtacatcctaagtgtgagaact 840  
QY 841 aatgctcgacaagaatgagccacataaaatcagaatttgacttgcacttgcagaagaagat 900  
DB 841 aatgctcgacaagaatgagccacataaaatcagaatttgacttgcacttgcagaagaagat 900  
QY 901 cacaagatcagccacacatgaagacatctgtgtgacctccagaatatctgcacagaagt 960  
DB 901 cacaagatcagccacacatgaagacatctgtgtgacctccagaatatctgcacagaagt 960  
QY 961 gttagaagaatagactatgagccagacagtagactgtgtggcctaggggtgtcactga 1020  
DB 961 gttagaagaatagactatgagccagacagtagactgtgtggcctaggggtgtcactga 1020  
QY 1021 tgaatgaatgtgtgagagttacaccttccacacacacagacacatgagaacactttgaat 1080  
DB 1021 tgaatgaatgtgtgagagttacaccttccacacacacagacacatgagaacactttgaat 1080  
QY 1081 aatatatgaagaagacattaaatttctctgaaacactcttccagatgcaaatcatctgt 1140  
DB 1081 aatatatgaagaagacattaaatttctctgaaacactcttccagatgcaaatcatctgt 1140  
QY 1141 ttcagagcctctgtataaagaatccaaataaagccttgtgtgagagccagatgagtaaa 1200  
DB 1141 ttcagagcctctgtataaagaatccaaataaagccttgtgtgagagccagatgagtaaa 1200  
QY 1201 agaaatlatgagacacagtttctctctgtgagtaaacgtgcagaatgtatataaaaa 1260  
DB 1201 agaaatlatgagacacagtttctctctgtgagtaaacgtgcagaatgtatataaaaa 1260  
QY 1261 gcttgaactccttttaaaccttaacatcctgtgagaagatagatatttttga 1320  
DB 1261 gcttgaactccttttaaaccttaacatcctgtgagaagatagatatttttga 1320  
QY 1321 agaatltacagctcagacatttacaataacacacacttgaataatagatgtgtat 1380  
DB 1321 agaatltacagctcagacatttacaataacacacacttgaataatagatgtgtat 1380  
QY 1381 ggaactcatgagacaatgagaagcgcgacatctccctcaatttccctactctgaaagt 1440  
DB 1381 ggaactcatgagacaatgagaagcgcgacatctccctcaatttccctactctgaaagt 1440  
QY 1441 acgagaataagtccttcaatctgttacttcaacttcaacttcaatttacttga 1500  
DB 1441 acgagaataagtccttcaatctgttacttcaacttcaacttcaatttacttga 1500  
QY 1501 tgaattcctgacatcacacagctccttaacatccttaacatccttaacatccttaacat 1547  
DB 1501 tgaattcctgacatcacacagctccttaacatccttaacatccttaacatccttaacat 1547

RESULT 2  
AAC77341  
ID AAC77341 standard; cDNA: 3285 BP.  
XX AAC77341;  
AC  
XX  
DT 08-FEB-2001 (first entry)

XX Human ORFX ORF2896 polynucleotide sequence SEQ ID NO:5791.  
DE  
XX  
KW Human: open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnery; antiparkinsonian; noctropic; neuroprotective;  
KW anticonvulsant; osteopathic; antihypertensive; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antineoplastic;  
KW antiviral; antibacterial; antifungal; antihemorrhagic; antihypertensive;  
KW antineoplastic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antineoplastic disease; coagulation;  
KW thrombosis; contraceptive; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2000058473-A2.  
XX  
XX 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000WO-US08621.  
XX  
XX 31-MAR-1999; 99US-0127607.  
XX 02-APR-1999; 99US-0127636.  
XX 05-APR-1999; 99US-0127728.  
XX 30-MAR-2000; 2000US-0540763.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shinkets RA, Leach M;  
XX  
XX WPI: 2000-602362/57.  
XX P-PSDB: AAB43132.  
XX  
XX Novel nucleic acids and peptides derived from open reading frame X,  
XX useful for treating e.g. cancers, proliferative disorders,  
XX neurodegenerative disorders and cardiovascular disease -  
XX  
XX Claim 5: Page 4956-4958; 5507pp; English.  
XX  
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX  
XX sequences have activities such as: cytostatic; hepatotropic; vulnery;  
XX osteoplastic; antiparkinsonian; noctropic; neuroprotective;  
XX osteoplastic; anticonvulsant; antihypertensive; immunosuppressant;  
XX immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
XX antidiabetic; hypotensive; dermatological; immunosuppressive;  
XX antineoplastic; antibacterial; antiviral; antihypertensive;  
XX antihypertensive; and antineoplastic. The sequences can be used for determining  
XX the presence of or predisposition to, or preventing or treating  
XX pathological conditions associated with an ORFX-associated disorder. The  
XX nucleic acids can be used to express ORFX proteins in gene therapy  
XX vectors. The proteins and nucleic acids may be used to treat cancers,  
XX proliferative disorders, neurodegenerative disorders, osteoarthritis,  
XX graft vs host disease, cardiovascular disease, diabetes mellitus,  
XX hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
XX erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
XX bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
XX allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
XX nocturnal haemoglobinuria, antineoplastic disease; to enhance  
XX coagulation; to inhibit thrombosis; and as a contraceptive.  
XX  
XX Sequence 3285 BP; 1028 A; 624 C; 690 G; 942 T; 1 other;

Query Match 99.9%; Score 1545.4; DB 21; Length 3285;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ggaagtcacatgaagcgaatgttaccattgtgaagaaggttgggttcagaagaggaggaga 60  
|||  
Db 465 gggagtcacatgaagcgaatgttaccattgtgaagaaggttgggttcagaagaggaggaga 524  
Oy 61 atataaaaaactgagagccaaagatacttcctttgagaagagatggcctcatcag 120  
|||  
Db 525 atataaaaaactgagagccaaagatacttcctttgagaagagatggcctcatcag 584  
Oy 121 atataaagaagaactcgaagatgttgatttaccattccctcccaacatttcagtgcc 180  
|||  
Db 565 atataaagaagaactcgaagatgttgatttaccattccctcccaacatttcagtgcc 644  
Oy 181 aaaaagcagtttaagaagaagaagcgaagccaaagccaaacattatcatcagtgct 240  
|||  
Db 645 aaaaagcagtttaagaagaagaagcgaagccaaagccaaacattatcatcagtgct 704  
Oy 241 ccagtggaactgtttatagagaacattcatgtatgatactccagaagaaaggaaaga 300  
|||  
Db 705 ccagtggaactgtttatagagaacattcatgtatgatactccagaagaaaggaaaga 764  
Oy 301 atggaagaagaactcgaagcgtgtgacgacagactcgaagcgaagcgaagcgaagc 360  
|||  
Db 765 atggaagaagaactcgaagcgtgtgacgacagactcgaagcgaagcgaagcgaagc 824  
Oy 361 gaattgtgacacactcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaagc 420  
|||  
Db 825 gaattgtgacacactcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaagc 884  
Oy 421 aaccacataaaaaagaagaacatgaatgattttacacatttgaacactcagtgaaag 480  
|||  
Db 885 aaccacataaaaaagaagaacatgaatgattttacacatttgaacactcagtgaaag 944  
Oy 481 cacttttgggaagttatttgggttcgagaagaagcgaagtggaataactatgctgaa 540  
|||  
Db 945 cacttttgggaagttatttgggttcgagaagaagcgaagtggaataactatgctgaa 1004  
Oy 541 gattctgaagaagaagaatcattatgcaagaagaatggaagcgaagcgaagcgaagc 600  
|||  
Db 1005 gattctgaagaagaagaatcattatgcaagaagaatggaagcgaagcgaagcgaagc 1064  
Oy 601 cagaatataaagaagaacatgacacatccttttlaacacatcctgaataatcctccagac 660  
|||  
Db 1065 cagaatataaagaagaacatgacacatccttttlaacacatcctgaataatcctccagac 1124  
Oy 661 aaaaagccgttgggttttggatgagaatgaaatgaagggcgagcgttttccatt 720  
|||  
Db 1125 aaaaagccgttgggttttggatgagaatgaaatgaagggcgagcgttttccatt 1184  
Oy 721 gtcgagaagaagggtgtctctctgagagcgaagcgaagcgttctatggttgaagaatgtctc 780  
|||  
Db 1185 gtcgagaagaagggtgtctctctgagagcgaagcgaagcgttctatggttgaagaatgtctc 1244  
Oy 781 tgccttggaactatcacaatccggaagaatgtgacgttgaacgttgaagaact 840  
|||  
Db 1245 tgccttggaactatcacaatccggaagaatgtgacgttgaacgttgaagaact 1304  
Oy 841 aatgctggaagaagaatggaagaatggaagaatggaagaatggaagaatggaagaat 900  
|||  
Db 1305 aatgctggaagaagaatggaagaatggaagaatggaagaatggaagaatggaagaat 1364  
Oy 901 caccagatgcaac 960  
|||  
Db 1365 caccagatgcaac 1424  
Oy 961 gttaaagaataatgacttgcgcgagcagtagacgttgcgagcagcagcagcagcagcagc 1020  
|||  
Db 1425 gttaaagaataatgacttgcgcgagcagtagacgttgcgagcagcagcagcagcagcagc 1484  
Oy 1021 tgaatgactgttggaggttacccttctacacacacacacacacacacacacacacacacac 1080  
|||  
Db 1485 tgaatgactgttggaggttacccttctacacacacacacacacacacacacacacacacac 1544  
Oy 1081 aatatataatggaagaacatataatttcctccggaacactccttcagatgtaaaatcatgtct 1140

Db 1545 aatataacgagagacatttaatttcctcgaaacccctcttcagatgcaaaatcattgct 1604  
Oy 1141 ttcaaggctcttgataaagatccaataaagccttggtagagggccgagatgcaaa 1200  
Db 1605 ttcaaggctcttgataaagatccaataaagccttggtagagggccgagatgcaaa 1664  
Oy 1201 agaaatcatgagacacagcttctctctgtagttaaactggcaagatgatatgataaaa 1260  
Db 1665 agaaatcatgagacacagcttctctctgtagttaaactggcaagatgatatgataaaa 1724  
Oy 1261 gcttgaacctctttaaaccctcaagtaacatctgagacagatagatatttgaaga 1320  
Db 1725 gcttgaacctctttaaaccctcaagtaacatctgagacagatagatatttgaaga 1784  
Oy 1321 agaattacagctcagacatttaacataacacacacccctgaaaaatagatgagatgct 1380  
Db 1785 agaattacagctcagacatttaacataacacacacccctgaaaaatagatgagatgct 1844  
Oy 1381 ggaactgcatggaacaatgagagcgcgccgcatctccctcaatttccctactctgcaagt 1440  
Db 1845 ggaactgcatggaacaatgagagcgcgccgcatctccctcaatttccctactctgcaagt 1904  
Oy 1441 agagagaataagctcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1500  
Db 1905 agagagaataagctcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1964  
Oy 1501 tgattcctgagacatcacagctccttagctcttacaatagcaggagca 1547  
Db 1965 tgattcctgagacatcacagctccttagctcttacaatagcaggagca 2011

## RESULT 3

AAC61592

ID AAC61592 standard; DNA; 2367 BP.

AC AAC61592;

DT 19-FEB-2001 (first entry)

DE DNA encoding a human kinase B-gamma polypeptide.

KM Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;  
KM phosphoinositide 3-kinase; insulin signalling;  
KM pleckstrin homology domain; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 10..1449 /tag= a  
FT /product= "kinase B-gamma polypeptide"

PW WO2000058446-A1.

XX 05-OCT-2000.

PD 23-MAR-2000; 2000WO-SE00571.

PF 25-MAR-1999; 99SE-0001115.

XX (PHAA ) PHARMACIA &amp; UPJOHN AB.

PA Attersand A;

PI WPI; 2000-647230/62.

DR P-PSDB; AAB19284.

XX Novel human protein kinase B gamma polynucleotides and polypeptides  
PT useful as probe or primers in polymerase chain reaction and to raise  
PT antibodies useful in diagnostic assays for detecting polypeptide  
PT expression -  
XX †

PS Claim 1: Page 16-19; 27pp; English.

XX The present sequence encodes a human protein kinase B gamma (PKB)  
CC polypeptide. PKB is activated by insulin or insulin growth factor 1.  
CC Lipid products of phosphoinositide 3-kinase act in insulin signalling  
CC by binding to pleckstrin homology domains of PKB. PKB polynucleotides  
CC may be used as a source of probes and primers. PKB polypeptides are  
CC used to raise antibodies, which are used in diagnostic assays. The  
CC polypeptides are also useful for screening for compounds which affect  
XX insulin signalling pathways.

SQ Sequence 2367 BP; 752 A; 444 C; 514 G; 657 T; 0 other;

## Query Match

99.8%; Score 1544.4; DB 21; Length 2367;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ggaatcatatgagcagatgtaccatttgaaagaaggttgggttcaagaaggagagaa 61  
Db 1 ggaatcatatgagcagatgtaccatttgaaagaaggttgggttcaagaaggagagaa 60  
Oy 62 tatataaaaaacttgagagcccaagatacttcttggagaacagatgctcatatagga 121  
Db 61 tatataaaaaacttgagagcccaagatacttcttggagaacagatgctcatatagga 120  
Oy 122 tataaagaagaaccccaagatgtggaattacattccctcaacacatttccagtggca 181  
Db 121 tataaagaagaaccccaagatgtggaattacattccctcaacacatttccagtggca 180  
Oy 182 aatgacagttatgaaaaacagaacgacccaagaacacacattataatcagatgttc 241  
Db 181 aatgacagttatgaaaaacagaacgacccaagaacacacattataatcagatgttc 240  
Oy 242 cagtgacacacgttatagaagaacattctatgtatgatacccgagaaaggagaa 301  
Db 241 cagtgacacacgttatagaagaacattctatgtatgatacccgagaaaggagaa 300  
Oy 302 tgagacagaagctatccagcgttgacagacagacgtcagagcgcaagaaggagaaatg 361  
Db 301 tgagacagaagctatccagcgttgacagacagacgtcagagcgcaagaaggagaaatg 360  
Oy 362 aattgtagtcacacttcaaaaaatgataatagagagagagagatggtatccctaca 421  
Db 361 aattgtagtcacacttcaaaaaatgataatagagagagagagatggtatccctaca 420  
Oy 422 acccatcataaaagaagaacatgaaatgtgactattgaaactactggttaaagc 481  
Db 421 acccatcataaaagaagaacatgaaatgtgactattgaaactactggttaaagc 480  
Oy 482 acttttggagaagattatttggttcgaagaagaagcggaatgaaatgactatgtaag 541  
Db 481 acttttggagaagattatttggttcgaagaagaagcggaatgaaatgactatgtaag 540  
Oy 542 attctgaagaagaagatcatatttgcaagaagtgaagtgcacacacttaactgaagc 601  
Db 541 attctgaagaagaagatcatatttgcaagaagtgaagtgcacacacttaactgaagc 600  
Oy 602 agagtataaagaacactagacatcccttttaacatccttgaatattccttccagaca 661  
Db 601 agagtataaagaacactagacatcccttttaacatccttgaatattccttccagaca 660  
Oy 662 aaagacgcttgggttgggttggatgataatgttaaggggagcgtgttttccattg 721  
Db 661 aaagacgcttgggttgggttggatgataatgttaaggggagcgtgttttccattg 720  
Oy 722 tcgaagagcggtgttctctgagagcccaacagcttctcatggtcgaatgttctct 781  
Db 721 tcgaagagcggtgttctctgagagcccaacagcttctcatggtcgaatgttctct 780  
Oy 782 gcttggactatcatctccgaaagaattgtatcgttgatcctaagttggaagatcta 841  
Db 781 gcttggactatcatctccgaaagaattgtatcgttgatcctaagttggaagatcta 840



Db 421 aaaaagaagcaaatgatttgatttgactatttgaaactactagtaagcactttggg 480  
 QY 491 aaagtattttgtctcgagagaagcaagtgtgaaataactatctatgtagatcttgaag 550  
 Db 481 aaagtattttgtctcgagagaagcaagtgtgaaataactatctatgtagatcttgaag 540  
 QY 551 aaagaagcaatatttgcagaagagtagagtgacacacttcaacttgaagcagagtatta 610  
 Db 541 aaagaagcaatatttgcagaagagtagagtgacacacttcaacttgaagcagagtatta 600  
 QY 611 aaagaagcaatatttgcagaagagtagagtgacacacttcaacttgaagcagagtatta 670  
 Db 601 aaagaagcaatatttgcagaagagtagagtgacacacttcaacttgaagcagagtatta 660  
 QY 671 ttgtgtttgtgtatgtgataatgttaattggggcgagactgttttccattgtctgagagag 730  
 Db 661 ttgtgtttgtgtatgtgataatgttaattggggcgagactgttttccattgtctgagagag 720  
 QY 731 cgggtgtctctcgagagaccgacacagcttctatgtgtcgagaaattgtctctgccttgag 790  
 Db 721 cgggtgtctctcgagagaccgacacagcttctatgtgtcgagaaattgtctctgccttgag 780  
 QY 791 tatctacattccgagaagttgtgtacgtgtatcctaagtttgagaatcttaagtcggagac 850  
 Db 781 tatctacattccgagaagttgtgtacgtgtatcctaagtttgagaatcttaagtcggagac 840  
 QY 851 aaagatgcccacataaataattacagatttgcagcttgcagaagaagggatcacagatgca 910  
 Db 841 aaagatgcccacataaataattacagatttgcagcttgcagaagaagggatcacagatgca 900  
 QY 911 gccacatgagaacatctgtgtgacctcagaataatctggtcaccagaagtgtagaagat 970  
 Db 901 gccacatgagaacatctgtgtgacctcagaataatctggtcaccagaagtgtagaagat 960  
 QY 971 aatgactatggtccgagcaatagactgtgtggcgctaggggtgtgtcatgtatgtaagatg 1030  
 Db 961 aatgactatggtccgagcaatagactgtgtggcgctaggggtgtgtcatgtatgtaagatg 1020  
 QY 1031 tgtgtgaggttacccttctcacaacccagagacatgagaacttcttaataatatttaag 1090  
 Db 1021 tgtgtgaggttacccttctcacaacccagagacatgagaacttcttaataatatttaag 1080  
 QY 1091 gaagacattaaattctcctcgaaacatctcttcagatgcaaaatcattgtcttcagggtc 1150  
 Db 1081 gaagacattaaattctcctcgaaacatctcttcagatgcaaaatcattgtcttcagggtc 1140  
 QY 1151 ttgataaagatcccaataaataagccttgtgtgagacccagatgagtgcaaaagaattatg 1210  
 Db 1141 ttgataaagatcccaataaataagccttgtgtgagacccagatgagtgcaaaagaattatg 1200  
 QY 1211 agacacagtttctctctctgtgagtaaacctggaagatgtatataataaagcttgcact 1270  
 Db 1201 agacacagtttctctctctgtgagtaaacctggaagatgtatataataaagcttgcact 1260  
 QY 1271 cctttaaaccctcaagtaacatctgagacagatagattatttgatgaagaatttaca 1330  
 Db 1261 cctttaaaccctcaagtaacatctgagacagatagattatttgatgaagaatttaca 1320  
 QY 1331 gctcagactattacaataaatacaccacttgataaataatgagagatgtatgtgactcatg 1390  
 Db 1321 gctcagactattacaataaatacaccacttgataaataatgagagatgtatgtgactcatg 1380  
 QY 1391 gacaatgagagcggtcgagatctcctcaatttccctactctgcgaagtgcagagataa 1450  
 Db 1381 gacaatgagagcggtcgagatctcctcaatttccctactctgcgaagtgcagagataa 1440

RESULT 5  
 AAA96637  
 ID AAA96637 standard; DNA; 1570 BP.  
 AC  
 XX AAA96637;  
 XX

DT 08-FEB-2001 (first entry)  
 DE DNA encoding a human Akt3 polypeptide.  
 XX  
 KW Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;  
 KW hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;  
 KW reperfusion injury; myocardial ischemia reperfusion injury; stroke;  
 KW liver damage; renal failure; organ transplantation; coronary artery; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 126..1523  
 FT CDS /tag= "a  
 FT /product= "Akt3"  
 XX  
 PN WO200056866-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 14-MAR-2000; 2000WO-US06574.  
 XX  
 PR 19-MAR-1999; 99US-0125108.  
 XX  
 PA (AVENTIS PHARM PROD INC.  
 XX  
 PI Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;  
 XX  
 DR WPI: 2000-638260/61.  
 DR P-PSDB: AAB19011.  
 XX  
 PT Novel AKT3 nucleic acid and proteins capable of preventing apoptotic  
 PT cell death induced by apoptosis stimulating kinase 1 useful for  
 PT treating myocardial infarction or ischemia reperfusion injury -  
 XX  
 PS Claim 3; Page 62-64; 73pp; English.  
 XX  
 CC The present sequence encodes a human Akt3 protein. Expression of Akt3  
 CC prevents apoptotic cell death induced by apoptotic stimulating kinase 1  
 CC (ASK1). The Akt3 polypeptide is useful for inhibiting cell death,  
 CC preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or  
 CC necrosis in a patient suffering from myocardial infarction or ischemia  
 CC reperfusion injury. The polypeptide is also useful for treating  
 CC myocardial infarction or ischemia reperfusion injury, where the  
 CC reperfusion injury is myocardial ischemia reperfusion injury or is  
 CC associated with stroke, liver damage, renal failure, organ  
 CC transplantation or coronary artery by pass grafting.  
 CC  
 CC Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 other:  
 XX  
 SQ  
 Query Match 88.2%; Score 1364.8; DB 21; Length 1570;  
 Best Local Similarity 98.4%; Pred. No. 0;  
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 gggagtcacatcagagcagatgttaccattgtgaaagaaggtgtgtcacaagaaggagaga 60  
 Db 116 gggagtcacatcagagcagatgttaccattgtgaaagaaggtgtgtcacaagaaggagaga 175  
 QY 61 atataaanaaacctgagagccaaagatctccttgaagaagatggtcattcatagag 120  
 Db 176 atataaanaaacctgagagccaaagatctccttgaagaagatggtcattcatagag 235  
 QY 121 atataaagaacacctcaagatgtgtattacttaccctcccaacaacttttcagtgagc 180  
 Db 236 atataaagaacacctcaagatgtgtattacttaccctcccaacaacttttcagtgagc 295  
 QY 181 aaaaatgcagtttaataaacaagacagacccaagaacacacattatataatcagatgtct 240  
 Db 296 aaaaatgcagtttaataaacaagacagacccaagaacacacattatataatcagatgtct 355  
 QY 241 ccagtgactactgttatagagagaacatttcaatgtatagatctccagaggaaggagaga 300

Db 356 ccaagtgaactactgttatagagagaacatttcattgtagatctccagaggaaggaaga 415  
 QY 301 atggacagaagctataccaggtctgttagacagacagactgcagaggcaagagaagaat 360  
 Db 416 atggacagaagctataccaggtctgttagacagacagactgcagaggcaagagaagaat 475  
 QY 361 gaattgttaattccaacttcgaattatagatagagggaagaatgatgaccttac 420  
 Db 476 gaattgttaattccaacttcgaattatagatagagggaagaatgatgaccttac 535  
 QY 421 aaccacataaaaagaagaacataatgatatatttgactatttgaaccttaagtaag 480  
 Db 536 aaccacataaaaagaagaacataatgatatatttgactatttgaaccttaagtaag 555  
 QY 481 caactttgggaagtatttctgttcgagagaaggaagtgcaaaatactatgtatga 540  
 Db 596 caactttgggaagtatttctgttcgagagaaggaagtgcaaaatactatgtatga 655  
 QY 541 gattctggaagaagaagatcatatgtcgaagaatgtagtgcacacactctaactaa 600  
 Db 656 gattctggaagaagaagatcatatgtcgaagaatgtagtgcacacactctaactaa 715  
 QY 601 cagagtatttaagaacacatacagatcccttttaacatccttgaaatattcctccag 660  
 Db 716 cagagtatttaagaacacatacagatcccttttaacatccttgaaatattcctccag 775  
 QY 661 aaaaagacgcttctgttctgtatggaataatgttaatggggcgagctgtttccatt 720  
 Db 776 aaaaagacgcttctgttctgtatggaataatgttaatggggcgagctgtttccatt 835  
 QY 721 gtcgagaagcggtgtctctcgaagaccgacacagcttctcattggtgcagaattctc 780  
 Db 836 gtcgagaagcggtgtctctcgaagaccgacacagcttctcattggtgcagaattctc 895  
 QY 781 tgccttggaactatctacatctcggaaagatgtgtacggtgatctcaagtctggaact 840  
 Db 896 tgccttggaactatctacatctcggaaagatgtgtacggtgatctcaagtctggaact 955  
 QY 841 aatgtcggacaaagatgtgcacataaaattacagaatttgagcttgcagaagaagat 900  
 Db 956 aatgtcggacaaagatgtgcacataaaattacagaatttgagcttgcagaagaagat 1015  
 QY 901 cccagatgcagccacacataagaacatctgttgcaactccgaataatctgcccagaag 960  
 Db 1016 cccagatgcagccacacataagaacatctgttgcaactccgaataatctgcccagaag 1075  
 QY 961 gttagaagaataatgactatggtcggagtagactgtgtgggcttaggggtgttcgtga 1020  
 Db 1076 gttagaagaataatgactatggtcggagtagactgtgtgggcttaggggtgttcgtga 1135  
 QY 1021 tgaatgagtgtgtgggaagttacacttctcaacaacgagaccatggaacttttgaat 1080  
 Db 1136 tgaatgagtgtgtgggaagttacacttctcaacaacgagaccatggaacttttgaat 1195  
 QY 1081 aatattaatggaagacataaatttctcgaacacactctctcgaatgcaaaatcattgct 1140  
 Db 1196 aatattaatggaagacataaatttctcgaacacactctctcgaatgcaaaatcattgct 1255  
 QY 1141 ttcagggctcttgataaagaatccaataaacgccttgtgtgaggaaccagatgtgcaa 1200  
 Db 1256 ttcagggctcttgataaagaatccaataaacgccttgtgtgaggaaccagatgtgcaa 1315  
 QY 1201 aaaaattatgagacacagtttcttctgtgagttaactgtgcaagatgtatatgataaaa 1260  
 Db 1316 aaaaattatgagacacagtttcttctgtgagttaactgtgcaagatgtatatgataaaa 1375  
 QY 1261 gcttgacctctctttaaaccctcaagtaacatctgagacagatcagatatttgaatga 1320  
 Db 1376 gcttgacctctctttaaaccctcaagtaacatctgagacagatcagatatttgaatga 1435  
 QY 1321 agaatttacagctcagactatacaataaacacacacacttgaaatatgatgtgaatgtat 1380  
 Db 1436 agaatttacagctcagactatacaataaacacacacacttgaaatatgatgtgaatgtat 1495

QY 1381 ggaactgcattggaacatgaga 1400  
 Db 1496 tggcatgcttggtaactgga 1515  
 RESULT 6  
 ID AAA89264 standard; cDNA; 1570 BP.  
 AC AAA89264;  
 XX  
 DT 28-MAR-2001 (first entry)  
 DE Human serine/threonine protein kinase Akt3 cDNA.  
 XX  
 KW AKT3; human; protein kinase; vascular endothelial growth factor;  
 KW VEGF; inducer; ischaemia; cardiomyopathy; angiogenesis; tumour;  
 KW gene therapy; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 126..1523  
 FT /\*tag= a  
 XX  
 PN MO200077190-A2.  
 PD 21-DEC-2000.  
 XX  
 PF 01-JUN-2000; 2000MO-US15098.  
 XX  
 PR 11-JUN-1999; 99US-0138724.  
 PR 03-NOV-1999; 99GB-0026058.  
 XX  
 PA (AVET ) AVENTIS PHARM PROD INC.  
 XX  
 PI Guo K, Ivashchenko Y, Clark K;  
 XX  
 DR WPI; 2001-025336/03.  
 DR P-PSDB; AAB19996.  
 XX  
 PT Inducing expression of vascular endothelial growth factor, useful for  
 PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal  
 PT ischemia or pulmonary ischemia, comprises administering a  
 PT serine/threonine protein kinase Akt protein -  
 XX  
 PS Example 1; Page 55-58; 67pp; English.  
 XX  
 CC The present sequence is that of cDNA coding for human Akt3 (see  
 CC AAB19996), a novel Akt isoform. Akt3 is a serine/threonine protein  
 CC kinase capable of inducing vascular endothelial growth factor  
 CC (VEGF) expression. The sequence was deduced from 2 cDNA clones  
 CC isolated from a human heart cDNA library using a human Akt3 partial  
 CC clone as probe. Akt3 is shorter than Akt1 (see AAB19997) and Akt2  
 CC (see AAB19998) and there is no significant homology between Akt3 and  
 CC Akt1 or Akt2 at the C-terminus of the molecules. A claimed method  
 CC of inducing expression of VEGF in a cell involves administering  
 CC Akt1, Akt2 or Akt3, or a nucleic acid encoding such a protein.  
 CC The cell is preferably from a patient suffering from an ischemic  
 CC condition, especially cerebrovascular, renal, pulmonary, limb or  
 CC myocardial ischaemia, or ischaemic, idiopathic or hypertrophic  
 CC cardiomyopathy. The result is beneficial collateral blood vessel  
 CC formation. A claimed method of inhibiting angiogenesis in a  
 CC patient suffering from a tumour, comprises inhibiting the level of  
 CC Akt activity in the patient, thereby inhibiting production of VEGF.  
 CC The method comprises introducing an Akt antisense nucleic acid,  
 CC an intracellular binding protein (e.g. a scrv) that specifically  
 CC binds the Akt protein, or a nucleic acid encoding a dominant  
 CC negative form of an Akt.  
 CC  
 SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 other;

Query Match 88.2%: Score 1364.8: DB 22: Length 1570;  
 Best Local Similarity 98.4%: Pred. No. 0:  
 Matches 1378: Conservative 0: Mismatches 22: Indels 0: Gaps 0;

QY 1 gggagatcatcatalgagcgatgttaccatgtgtbaagaaggttgggttcagaagaaggagga 60  
 |||||  
 Db 116 gggagtcacatcatgagcgatgttaccatgtgtbaagaaggttgggttcagaagaaggagga 175  
 QY 61 atatatataaaacttgagcgccaagatacttcttcttgagaagacagatggcctcatctaga 120  
 |||||  
 Db 176 atataataaaacttgagcgccaagatacttcttcttgagaagacagatggcctcatctaga 225  
 QY 121 atataagaagaaccctcaagatgtgatttacccttaccctcaacaacttccatggc 180  
 |||||  
 Db 236 atataagaagaaccctcaagatgtgatttacccttaccctcaacaacttccatggc 295  
 QY 181 aaaaatgcagtttaataaacaagacgaaccaagccaacacattataatcagatgtct 240  
 |||||  
 Db 296 aaaaatgcagtttaataaacaagacgaaccaagccaacacattataatcagatgtct 355  
 QY 241 ccagtgactactgttatagagaagaacattctatgtatagatcccgagagaaggaga 300  
 |||||  
 Db 356 ccagtgactactgttatagagaagaacattctatgtatagatcccgagagaaggaga 415  
 QY 301 atgacagaagaagctatccagctgttagacagacactgcagaggcaagaagagagaat 360  
 |||||  
 Db 416 atgacagaagaagctatccagctgttagacagacactgcagaggcaagaagagagaat 475  
 QY 361 gaattgtatgtccaaacttcaacaaatgtataatagagaagagaatgtgctctac 420  
 |||||  
 Db 476 gaattgtatgtccaaacttcaacaaatgtataatagagaagagaatgtgctctac 535  
 QY 421 aaccctatcaataaagaagaacaaatgtatgttgaactatttgaactactatgtataagg 480  
 |||||  
 Db 536 aaccctatcaataaagaagaacaaatgtatgttgaactatttgaactactatgtataagg 595  
 QY 481 caattcttggaagaagttatttgttctgagagaagcgcaagtggaataatacatgtcttga 540  
 |||||  
 Db 596 caattcttggaagaagttatttgttctgagagaagcgcaagtggaataatacatgtcttga 655  
 QY 541 gattctgaagaagaagatcatatgtcaaaagatgaagtgcacacacttaactgaag 600  
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 Db 716 cagaagattaaagaacacactagacatcccttttaacatcccttgaatatcttccacagac 775  
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 Db 776 aaaaagacgcttctgttcttctgtatgttaatgttgaggcgagcgttcttccatt 835  
 QY 721 gtcgagaagcggtgttctctctgaagacgcgacacgcttctatgtgtgcagaatgtctc 780  
 |||||  
 Db 836 gtcgagaagcggtgttctctctgaagacgcgacacgcttctatgtgtgcagaatgtctc 895  
 QY 781 tgccttgagactatcatctacccgaaagatgtgtacccggtacatcaagtgtgaagatct 840  
 |||||  
 Db 896 tgccttgagactatcatctacccgaaagatgtgtacccggtacatcaagtgtgaagatct 955  
 QY 841 aatgctgcacaagaatgcgcacataaaattacagatttggacttgcacaagaaggat 900  
 |||||  
 Db 956 aatgctgcacaagaatgcgcacataaaattacagatttggacttgcacaagaaggat 1015  
 QY 901 cacagatgcagccacatggaagacattctgttgacactccagaatatctgcaccagagt 960  
 |||||  
 Db 1016 cacagatgcagccacatggaagacattctgttgacactccagaatatctgcaccagagt 1075  
 QY 961 gttagaagataatgactatgtgcgagcagtagaactgttgaggccttaggggttctatgta 1020  
 |||||  
 Db 1076 gttagaagataatgactatgtgcgagcagtagaactgttgaggccttaggggttctatgta 1135

QY 1021 tgaatgatgtgtggaggttacccttcttcaacaaccagacatgagaacatttctgaatt 1080  
 |||||  
 Db 1136 tgaatgatgtgtggaggttacccttcttcaacaaccagacatgagaacatttctgaatt 1195  
 QY 1081 aatatcaatggaagacatttaaatcttcttcgaacacctcttccatgacaaatcatgtct 1140  
 |||||  
 Db 1196 aatatcaatggaagacatttaaatcttcttcgaacacctcttccatgacaaatcatgtct 1255  
 QY 1141 ttcaaggcctcttgaataaagatccaaataaagccttggctggaggaaccagatgtcaaa 1200  
 |||||  
 Db 1256 ttcaaggcctcttgaataaagatccaaataaagccttggctggaggaaccagatgtcaaa 1315  
 QY 1201 agaaattatgagacacagttcttctctctgtgagtaaaacttgcgaagatgtatagataaaaa 1260  
 |||||  
 Db 1316 agaaattatgagacacagttcttctctctgtgagtaaaacttgcgaagatgtatagataaaaa 1375  
 QY 1261 gcttgtactctctttaaaccctaaagtaacatcttgagacagatagatatttgaatga 1320  
 |||||  
 Db 1376 gcttgtactctctttaaaccctaaagtaacatcttgagacagatagatatttgaatga 1435  
 QY 1321 agaatataagctcacactatatacaaacacacttgaaaaatagatgagatgtgtat 1380  
 |||||  
 Db 1436 agaatataagctcacactatatacaaacacacttgaaaaatagatgagatgtgtat 1495  
 QY 1381 ggaactgacatgacacatgaga 1400  
 |||||  
 Db 1496 tggcatgtcgtggtaactgga 1515

RESULT 7  
 AAA09078  
 ID AAA09078 standard; DNA; 2626 bp.  
 XX  
 AC AAA09078;  
 XX  
 DT 10-AUG-2000 (first entry)  
 XX  
 DE Wild type murine Akt coding sequence.  
 XX  
 DE Akt: protein kinase B; serine-threonine kinase; proto-oncogene; cardiant;  
 KW Inhibitor; apoptosis; cell death; antiapoptotic; muscular activator; ss.  
 KW  
 OS Mus musculus.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 284..1726  
 FT /tag= a  
 FT /product= protein\_kinase\_B  
 XX  
 PN WO200020025-A2.  
 XX  
 PD 13-APR-2000..  
 XX  
 PF 29-SEP-1999; 99WO-US22633.  
 XX  
 PR 02-OCT-1998; 98US-0102740.  
 XX  
 PA (SELI-) ST ELIZABETH'S MEDICAL CENT IMC.  
 XX  
 PI Walsh K;  
 XX  
 DR WPI: 2000-303639/26.  
 DR P-PSDB: AA92223.  
 XX  
 PT Treating myocardial infarction or conditions associated with increased  
 PT apoptotic cell-death of vascular endothelial cells or skeletal  
 PT myocytes comprises administering Akt (also termed Protein Kinase B  
 PT (PKB) molecule  
 XX  
 PS Disclosure: Page 69; 71pp; English.  
 XX  
 CC The invention concerns methods of treating myocardial infarction, which  
 CC comprise administering to a subject an Akt (Protein Kinase B) molecule







KM RAC protein kinase; pleckstrin homology domain; signal modulator;  
KM screening; fluorescence; human; ss.  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 199..1641  
XX FT /\*tag= a  
XX FT  
XX MO972217-A1.  
XX  
XX  
XX PD 26-JUN-1997.  
XX  
XX PF 05-NOV-1996; 96MO-EP04814.  
XX  
XX PR 15-DEC-1995; 95GB-0025705.  
XX PR 15-DEC-1995; 95GB-0025703.  
XX  
XX PA (NOVS ) NOVARTIS AG.  
XX  
XX PI Frech M, Hemmings BA;  
XX WPI: 1997-341705/31.  
XX DR P-PSDB; AAM18515.  
XX  
XX PT Screening for modulators of signal pathways - by incubation with  
XX PT fluorescently labelled pleckstrin homology domain of signalling  
XX PT molecule and detecting changes in fluorescence  
XX  
XX PS Disclosure: Page 16-20; 39pp; English.  
XX  
XX CC This cDNA sequence encodes human RAC protein kinase (AAM18515). The  
XX CC pleckstrin homology (PH) domain of RAC protein kinase can be used  
XX CC in a claimed method for screening for modulators of signal pathways.  
XX CC This involves: (a) incubating the test compound with the PH domain  
XX CC of a signalling molecule which is capable of fluorescence; and (b)  
XX CC determining phospholipid-induced changes in fluorescence, indicating  
XX CC a functional interaction between the compound and the PH domain.  
XX CC Fluorescence is preferably associated with the Trp-223 of RAC protein  
XX CC kinase PH domain. The method allows screening for compounds which  
XX CC modulate signal pathways involving the serine/threonine kinase RAC  
XX CC and can especially be applied to protein kinases and their  
XX CC substrates, which are implicated in intracellular signalling and  
XX CC growth control. The high affinity binding of phospholipid to the PH  
XX CC domain of signalling molecules suggests that this domain is a  
XX CC membrane anchor for the molecules: molecule interactions with the  
XX CC cell membrane are important for their stable interaction with  
XX CC membrane-bound partners in signalling pathways, so that disruption  
XX CC of the interaction modulates the signalling effect. By measuring  
XX CC this modulation (which may be down-regulation for stimulatory  
XX CC interactions or upregulation for inhibitory interactions) compounds  
XX CC which can have an effect can be identified e.g. agents which cause  
XX CC conformational changes in the PH domains or which compete directly  
XX CC for binding of the PH domain to the cell membrane. A claimed method  
XX CC for production of the RAC protein kinase PH domain in a bacterial  
XX CC cell comprises expressing a nucleic acid sequence encoding the PH  
XX CC domain having at least 3 hydrophilic amino acids (preferably Lys)  
XX CC residues joined directly at its C-terminus (see AAM18519).  
XX  
SQ Sequence 2610 BP; 537 A; 752 C; 781 G; 540 T; 0 other:

Query Match 46.5%; Score 719.2; DB 18; Length 2610;  
Best Local Similarity 70.3%; Pred. No. 7.1e-185;  
Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

Oy 5 gtcacatgagcagatgtacacatgtgaagaaggttggtcagagaagggagaatat 64  
Db 193 ggcaccatgagcagcagtggtcatgtggaagggttggtcgaacaacgaggagatc 252

Oy 65 ataaaaactgagagccagaatactcttctgaagacagatgctcattcagaatat 124  
Db 253 atcaagactgtgcgcacgcactactctcctcgaagaatgagacacttcttgctac 312

Oy 125 aagaagaaccccaagatgtgatttacccta---tccctcaacaactttcaatggca 181  
Db 313 aagagcgcgcgcagagatgtgtgccaacagtgtagctccctcaacaacttctgtgcg 372

Oy 182 aatgtccagttaatgaacaacagacgacccaagaacacacattataatcagatgtc 241  
Db 373 cagtgcagctgtatgaagcgcgagcccgcccaacaacttcatcctgcgtcgtc 432

Oy 242 cagtgtactatgttatagagagaacattctcatagatactccagagaaaggaagaa 301  
Db 433 cagtgtaccactgtcatcgaacgcacattccatgtgagagactcctgagagagag 492

Oy 302 tggacaagaagctatccagcttgaagcagaacgctgcgaggaaggaaggaagaa 361  
Db 493 tggacaaccgcacccagactgtgtcgtgcgcctcaaaagcagaaggaaggaagatg 552

Oy 362 aattgtatgccaacttcaacaataatagatagagaggaagatgtatcctctaca 421  
Db 553 gacttcgcgtgcgtgcctaccagtgacaactcagggcgtgaagatgaggtgtccctg 612

Oy 422 acccatc---ataaagaagaacaatgaatgtattgtactatttgaactactagtaa 478  
Db 613 gccaaagcccaagcaccgcgtgacccatgaacgaggttgatgactgaagctgtgycgaag 672

Oy 479 ggcacttttggaaagttatttggttcgaagagaagcgaatgtgaaataactatgtatg 538  
Db 673 ggcacttttggaaagttatttggttcgaagagaaggaagcgaacgctgtactacgcat 732

Oy 539 aagattctgaagaagaagatctatttgcagaagatgagtgccacacttaactaa 598  
Db 733 aagatccctcaagaagaagatctatgtgcgaagcaggggtgcccacactacccag 792

Oy 599 agcagaatattaagaacacactagacatcccttttaacatcttgaataatctctccag 658  
Db 793 aaccggtcctcagacacactcagcacccttcccaacgcccctgaagtaactcttcag 852

Oy 659 acaaaaagacgtttgtttgttgtgataatgttaatgggggcgagctgtttccat 718  
Db 853 aaccagcgcgtctgtgtgtgtcattgtgagtagcgaacgaggggcgagctgttctcac 912

Oy 719 ttgtcgaagagcgggtgttctctcagagaccgacacgttctatgagtgacaatgttc 778  
Db 913 ctgtcccggaacggtgtgttctccgaagaacgggccgtctctatggcgtgagatgtg 972

Oy 779 tctgcttggactatcaatcaccgaaaga---ttgtgtaccgtgattcgaattggag 835  
Db 973 tcaagccctgactactcgtcactcgcgagaagaacggtgtgtacccggagactcaagctgag 1032

Oy 836 aatctaagtctggacaagaatgagccacataaataatcaagatttggacttgcagaaga 895  
Db 1033 aacctcaatgtgaaagaagcagggcacttaagatacacagacttggcgtgtgcagaag 1092

Oy 896 gggatcaagaatgagcagccacatgaagaacatctctgtgcaccccgagtaactgtgcc 955  
Db 1093 gggatcaagaagcaggtgtccacccatgaagacatttgcgcaccccgagtaactgtgcc 1152

Oy 956 gagggttagaagaatagactatgacccgagcagcagctggtgagggcctgaggtgttc 1015  
Db 1153 gagggtcgtgaggaacatgactacggtgcgtgagcaggtgtggtggtggtggtgtc 1212

Oy 1016 atgtatgaatgatgtgtggtggtgttaccttctcaacaccagagacatgagaactttt 1075  
Db 1213 atgtatgaatgatgtgtggtggtgttaccttctcaacaccagagacatgagaaggtttt 1272

Oy 1076 gaattaataatgaaagacatlaatttccctgaacaacotcttcagatgacaatacca 1135  
Db 1273 gaggctacatccatcctcagagagatcccgcttcccgccagcgtgtgtcccgagggccaa 1332

Oy 1136 ttgcttcaaggtctcttgaataaagatccaaataaacgccttgtgtgagagcagatgt 1195  
Db 1333 ttgcttcaaggtctctcagaagaagaccccaagcagaggtgtgtggtggtggtcgcagagac 1392

Oy	1196	gcaaaagaaatitgagacacgaatttctctcgcgagtaacttgcgaagatgatatgat	1255
Db	1333	gccaaaggagatcacagacgcctgcctctcttcgcggatcgtgtgtgcgaacacgttgcacag	1452
Oy	1256	aaaaagcttctaccctctttaaaccctcaagtacactctgcagacagatattagatatctt	1315
Db	1453	aagaagctcagccaccccttcaagcccccagtcagtcgtagagatctgacacccagtatctt	1512
Oy	1316	gattaaagatttcacgtctcgaactattacataaaccccccctgaaataatagatgat	1375
Db	1513	gattcaggagattccacagcgcacagatcatcatcaacacacccgcgacaa----gatgac	1566
Oy	1376	gatttgacctgcacgtacaaatgagagcgcgccgcatatttccctcaatttctctactctcga	1435
Db	1567	agcatcgtgagtgtgtgcacagcgcgacgagccccaattcccccagttctctactcgcgc	1626
Oy	1436	agtgcagcagatataatgc	1453
Db	1627	agcacgacgcgccttgaagc	1644

**RESULT 10**

AAT67135  
ID AAT67135 standard; cDNA to mRNA; 2610 BP.

AC AAT67135;

DT 12-DEC-1997 (first entry)

Human RAC protein kinase alpha cDNA

KW RAC protein kinase C-terminal binding protein; CTBP; modulator, RNA strand translocation; insulin; diabetes; cell growth; fetal

glycogen; therapy; diagnosis; ss.

OS Homo sapiens.  
xy

FH	Key	Location/Qualifiers
EM	CDS	100 1641

FT  
XX

PN WO9718303-A1  
XX

PD 22-MAY-1997.  
YY

PF 05-NOV-1996;  
XY

PR 15-DEC-1995;  
PR 16-NOV-1995;

XX  
XX  
PA (NOV 1) NOYAF

XX  
DT Hemming BA:

XX  
MPY: 1007-200

DR P-PSDB; AAW17

PT	RAC protein	PT	RAC protein
1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
8	8	8	8
9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
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94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

PT insulin media

PS Disclosure; F

CC This cDNA seq

of glycogen

CC pathways, which

CC treatment of

CC deficiency and

CC used in a cla

CC	Insulin mediated intracellular signalling. Activated mutant
CC	RAC-PI3K (see AAM17983-85) may also be used in such screenings.
XX	
XX	Sequence 2610 BP; 537 A; 752 C; 781 G; 540 T; 0 other;
Query Match	46.5%; Score 719.2; DB 18; Length 2610;
Best Local Similarity	70.38; Pred. No. 7,1e-185;
Matches 1025; Conservative	0; Mismatches 418; Indels 15; Gaps
OY	5 gtcatcatgagcgaatgttaccatgttgaagaagagcttgggtcttcagaagaaggaggagaatcat 64
Db	193 ggcacacatgagacgcgcgcgtgctatgtgaagagagtggtgctgcacaaagaaggagatcac 252
OY	65 ataaaaaacctggagagccaagatacttccttttgaagacagatggtcattcatatagaatat 124
Db	253 atcaagacctggcgcgcacgcctactctctctccaagaatgatgtagccacttcatgtgtcac 312
OY	125 aaagagagaacctcaagtatgtgttatcctta---tccctcaaacactttcagtgtgca 181
Db	313 aagagcgcgccgcagagatgttgacaacacgctgaaggtctccctcaacaactctctctgtag 372
OY	182 aatgtccagattgaataaacagcaacgcgaacgaacgaacacatttaactcagaatgtctc 241
Db	373 cagtgccgcctgtatgagaagcggagcggtcccccgcacaaaccttcatctccgcgtcgt 432
OY	242 cagtgtactactgttatatagaagagacaattcatgtatgaatactccagaagaaaggagagaa 301
Db	433 cagtgtaccactgtcatctcgaacgccttccatctgtgagatctctctgtagagcgcgagag 492
OY	302 tggacagaagatcatccaggtctgtatgacagaagaagcttcgacagagcaagaagaagagaaatg 361
Db	493 tggacaacaacgcctacccagactgtgtctgacgcgcctcaagaagaagaagagagagagatg 552
OY	362 aattgtaatccaaacttcaacaatgtataatcatatgagagagagaaatgtatgtctctca 421
Db	553 gacttcgcgtctgggtctcaaccacagtgaaatactcaggggtcgaagaagatgtgagtgccgtg 612
OY	422 acccatc---ataaagaagaacacatgatattgtacttgcataatttgaactactagtaaa 478
Db	613 gccaaagcccaagcaccgcgtgtgacacatgaacgaattgtgaattaccctgaagctctgttcg 672
OY	479 ggcaccttttggaagatatttttgggtctcggagaaagagcaagtggaataatacatgtctatg 538
Db	673 ggcaccttcgcgaagagtgatctccgtgtgaagagaaagagccaaggtccgcctacacgcctatg 732
OY	539 aagatcttgaagaagaagatcatattatgtgcaaaagatctgaagctgcacacactcaactgaa 598
Db	733 aagatcctccaagaagaagatcatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 792
OY	599 agcagagatataaagaacacactagacatcccttttlaacatacctcttgaataatctcttcag 658
Db	793 aaccggtctctgcgaagaactccagagcacccttctctctcaagcccttgaaagtacttcttcag 852
OY	659 acaaaagacggtttgtgtttttgtgtatgtgaatagttaatgtggtgggcgagctgttttccat 718
Db	853 aaccacagacgcgcctctgtctgtcatgtgaatgaatgacgaacgggggcgaagctgtcttcacac 912
OY	719 ttgttcggagagggcggtgtctctctgtgaagacggcaacagttttctatgtgttcagaaaatttgc 778
Db	913 ctgtctcccggaacgtgtgttctctccgaagacgcgggcgcgtctctcatgtgcgtcgaagatgtg 972
OY	779 tctgccttgcgaactctacatctccggaanaa---ttgtctacgctgtatctcaagcttgag 835
Db	973 tcaagcctcgtgactctaccctgcacactcggagaaagatgtgtgtacccgggaactcaagcttgag 1032
OY	836 aatctaattgttgcacaaagatgtgcacataaaaaattacagatttttgaccttgcagaagaa 895
Db	1033 aacctcatgtctgacaaagcgcgacacataaagatcatcagaacttcgggtgtgtgcaagaag 1092
OY	896 gggtatcacagatgtgagccaccatgtgaagaatattctgtgtgcaactccagaataatctgtcacca 955
Db	1093 gggtatcaagagcgggtgtccacatgtgaagaacttttggtagacacactgtgatactgtgccc 1152

QY	956	gaggctgtctgaagaataatgactctatgcccgaagcaagtcagctggttggtgacctaggggtctc	1015
Db	1153	gaagtcgtggaagacacatgactctacggccglgacagtcagtctgggggctggccgttgc	1212
QY	1016	atgcatbaaattgctgtgtgtgggaggttaaccttctcacaacagaccatgagaaactttt	1075
Db	1213	atgtaacagatctgctgtgcgtctgcgcctctctacaacagaccatgagaaagctttt	1272
QY	1076	gaatcatatctaattgagacatctaattcttcgcgaacatctctccagatgacaaatc	1135
Db	1273	gagctatctctcatgtgagagagatccgctctccgcgcagctgtgtcccgagcccaatcc	1332
QY	1136	tgtcttccaagggtctctgtataaaggatccaaataaacgcgttgtgtgagagaccagatgat	1195
Db	1333	tgtcttccaagggtctctgtataaaggatccaaataaacgcgttgtgtgagagaccagatgat	1392
QY	1196	gcacaagaaattagagacacagttctctctctgtgagtaactggaagatgtatagat	1255
Db	1393	gccaaaggagatcatgcatgcctctctctgttcgcgtatctgtgtgcagacagtcgtacag	1452
QY	1256	aaaaagtgctacctctctttaaactctcaagtaagaactctgaaacacagatactagatattt	1315
Db	1453	aagaagctgacgccacaccttcaagcccacggatccgtgcgtgagatccagaaacccagatattt	1512
QY	1316	gataaagaattacaagctcagactatctacaataaacaccgcctgaaanaatatgatagatg	1375
Db	1513	gatgtagagattcacgcccagatgataccacatcaaccacactgtaccaa-----gatgac	1566
QY	1376	gatactgacatcgtacaaatgagagtcgagccgcatcttccctcaatttctctactctcga	1435
Db	1567	agcatgtagatgctgtgagacagcgagccccactctccccagttctctctactctgcgc	1626
QY	1436	agctgacgacgaataaattc	1453
Db	1627	agcagcagcgccctgtacg	1644

RESULT	11
AA241177	
ID	AA241177 standard; cDNA; 2610 BP.
XX	
AC	AA241177;
XX	
DT	26-JAN-2000 (first entry)
XX	
DE	Human AKT-1 encoding cDNA.
XX	
KW	Identification; genetic target; gene modulation; human; probe; antisense oligonucleotide; phosphorothioate; PCR primer; nucleotide sequence-based technology; antisense drug discovery; target validation; ss.
XX	
OS	Homo sapiens.
XX	
FN	W09953101-A1.
XX	
PD	21-OCT-1999.
XX	
PE	13-APR-1999; 99MO-US08268.
XX	
PR	13-APR-1998; 98US-0081483.
PR	28-APR-1998; 98US-0067638.
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	Consert LM, Baker BF, McNeil J, Freier SM, Sasamor HM, Brooks DG; Onasi C, Wyatt JR, Borchers AH, Vickers TA;
XX	
DR	WPI: 1999-620446/53.
DR	P-PSDB: AAY52706.
XX	
TT	Identifying compounds which modulate expression of nucleic acids, used

to provide compounds having defined physical, chemical or bioactive properties, e.g. antisense activity -

A method has been developed of defining a set of compounds that modulate the expression of a target nucleic acid (tNA) sequence via binding of the compounds with the tNA sequence. The method comprises generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual compounds with the tNA according to defined criteria. Also described are: (1) a method of defining a set of oligonucleotides (ONS) that modulate the expression of a tNA sequence via binding of the ONS with the tNA sequence comprising generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual ONS with the tNA according to defined criteria; and (2) a method of defining a set of compounds that modulate the expression of a tNA sequence via binding of the compounds with the tNA. The methods can be used for the generation and identification of synthetic compounds having defined physical, chemical or bioactive properties. Information gathered from assays of such compounds is used to identify nucleic acid sequences that are tractable to a variety of nucleotide sequence-based technologies, e.g., antisense drug discovery and target validation. AAZ40852 to AAZ41220, and AAY52701 to AAY52706, represent sequences used in the exemplification of the present invention.

SQ Sequence 2610 BP; 537 A; 752 C; 781 G; 540 T; 0 other;

Query Match	46.58;	Score 719.2;	DB 20;	Length 2610;
Best Local Similarity	70.38;	Pred. No. 7.1e-185;		
Matches 1025; Conservative	0;	Mismatches 418;	Indels 15;	Gaps 4

QY	5	gtctatcatgaa	cgcgtatg	tcatccat	tgtgtga	aaagaagttt	ggtgtctc	gaagaagg	ggaatat	64
Db	193	ggcaccatgaa	cgcagtcg	tgtcatct	tgttga	aagaaagttt	gtgtctc	gaacaacga	ggaggat	252
QY	65	ataaaacttga	agcccaagtact	cccttlttga	agacagtgtc	tcatcatg	gatat	124		
Db	253	atcaagacct	tgtcggtccacg	ctacttctc	tctctca	gaatgtat	gtgacctt	catgtgtac	312	
QY	125	aaaggaac	cttcaagat	tgttgatt	taactta	ctta---tcc	ctccaac	actttc	agtgca	181
Db	313	aagagcg	cgccgac	gatgtgtg	acaacgtg	agcttcc	ctccaac	acttctct	gtgcg	372
QY	182	aaatgtcc	agttat	gtga	aaacga	agaccaca	acattat	taatcat	gtgtc	241
Db	373	cagttcc	agctgtat	gtga	aaacga	agcccgcc	gccaac	acttcat	catctgc	432
QY	242	cagtgact	atctgt	tatg	agagaa	acttcat	tgtat	atactc	agagaa	301
Db	433	cagtgac	ctacgt	ctcat	tgaa	agcaactt	ccaatgt	gtgagat	ctcttg	432
QY	302	tgaaga	agacat	cgtctc	agacgt	ctcga	agacgt	ctcga	agagag	361
Db	493	tgaaca	acgcac	ctcatc	agactgt	gtctga	cggtc	ctcaag	agcgag	552
QY	362	aattgt	agtc	ccaact	ccaata	tgtata	atbaga	agaga	gatgtg	421
Db	553	gacttc	cggtct	ggtctcc	ccagtg	acaactc	agagcg	gtctga	agagat	612
QY	422	accctc---	taaa	aga	aaaga	acat	atgat	attt	taactt	478
Db	613	gccaa	gccc	aaagca	ccggtg	acaatga	agca	agttt	gtagta	672
QY	479	ggcactt	cttctg	aaagtatt	tttctgt	ctcga	agagaa	caagttg	gaaata	538
Db	673	ggcactt	ctcgtc	gaaggtg	atctctgt	gtga	aggaag	gccaag	gcgcgt	722
QY	539	aagat	cttga	agaaga	agatcat	tattgt	caaga	agatgt	gcacac	588
Db	733	aagat	cttca	gaaga	agaaat	catctgt	ctgc	caaga	acagat	792

QY 599 agcagatattaaagaactagacatccctttttaacatcccttgaaataatctccacag 658  
 DB 793 aaccgctccctgcagaactccacagcacccttcctccacagccctgactccttcacag 852  
 QY 659 acaaaagaccgtttgtgtttgtgatggaatgttaatggggcgagcgtttttccat 718  
 DB 853 acccaagaccgctcctgtcttgcatagtggaatgacccaagcgagcgagcgttctccac 912  
 QY 719 ttgtcgaagaagcggtgtctctctgagagcagcacaagttctataggtcagaatgttc 778  
 DB 913 ctgtcccggaacgtgtgtctctcgagagccggtccgtctcatgtgcgtgagatgtgtg 972  
 QY 779 tctgccttgagctatctacatctccggaaga-----tggtaccgtgtatctccaagttggag 835  
 DB 973 tcaagccctgacacccagcctcgcggaagaacgtgtgtgtacccggaaccccaagcttggag 1032  
 QY 836 aatcatagtctgcacaagaatgcccacataaaataatcaaatcttgacttgcagaaga 895  
 DB 1033 aacctatgtctgcacaagaagcggtccacataaagatacagaacttcgggtctgtcagaagag 1092  
 QY 896 ggagatcacagatgcagccacatgaaagacatctgtgtgcacatccagaataatctgcacca 955  
 DB 1093 ggagatcaagagcgtgtccacacatgaaagacatctgtgtgcacacactgtgacacccgtgc 1152  
 QY 956 gaaggtttgaagaataatgactatgtgcgcagcagtagactggtgtgggcttaggggtgttc 1015  
 DB 1153 gaaggtctggaagacatgactacgtgcgtgcgtgtgactgtgtgtgtgtgtgtgtgtgt 1212  
 QY 1016 atgtacgaataatgactgt 1075  
 DB 1213 atgtacgaataatgactgt 1272  
 QY 1076 gaataatattaaatgaaagacatlaattctctgcagacactctctcagatgcaaaaatca 1135  
 DB 1273 gactcatctcctcagagagatcgcgtctccgcgcagcgttgcgcgcagagcgaagcttc 1332  
 QY 1136 ttgcttccaggtctctgttaagaagatccaataaagccttgggtgtgagagacagatgat 1195  
 DB 1333 ttgcttccaggtctctgttaagaagatccaataaagccttgggtgtgagagacagatgat 1392  
 QY 1196 gcaaaagaataatgaaagacagttctctctgtgagtaaaactgtgcaagagatgtatgtat 1255  
 DB 1393 gccaagagatgactgagatcgtctctgtgcgtgtatcgtgtgtgcaagacgtgtatgtat 1452  
 QY 1256 aaaaagctgttactccttttaaacctcaagtaacatctgcagatagatagatattt 1315  
 DB 1453 aagaagctcagccacccttcaagcccgagtcagcgtgcagatgacacccagatattt 1512  
 QY 1316 gactgaagaattacagctcagatctataataacacccctgaaataatagatgagat 1375  
 DB 1513 gatgaagagtcacagccagatgacacacacacacacacacacacacacacacacacacac 1566  
 QY 1376 ggtatgactgtcagatgagacatgagagcgccgacatttccccaatttctcactatgta 1435  
 DB 1567 agcatgtgagtggtgtgacgcgagcgacgcccccaattccccaatttctcactatgta 1626  
 QY 1436 agtgcagcgaataagtc 1453  
 DB 1627 agcagcagcgctgagcg 1644

## RESULT 12

AAZ22190  
ID AAZ22190 standard; DNA; 2610 BP.

AAZ22190;

26-NOV-1999 (first entry)

Human Akt-1 DNA sequence.

Human Akt-1; antisense; diagnostic; therapeutic; prophylaxis;  
infection; inflammation; tumor formation; ss.

Human Akt-1; antisense; diagnostic; therapeutic; prophylaxis;  
infection; inflammation; tumor formation; ss.

XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH CDS 199..1641  
 FT CDS /tag= a  
 PN US9598773-A.  
 PD 28-SEP-1999.  
 PF 17-DEC-1998: 98US-0212771.  
 PR 17-DEC-1998: 98US-0212771.  
 XX (ISIS-) ISIS PHARM INC.  
 PA Monia BP, Cowser LM;  
 PI WPI: 1999-561048/47.  
 DR P-PSDB: AAY33999.  
 XX Antisense compounds complementary to Akt-1 useful for, e.g.  
 PT diagnostics, therapeutics and as research reagents -  
 XX Example 13; Columns 43-46; 32pp; English.  
 CC The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Akt-1. The antisense compounds may be  
 CC used for diagnostics, therapeutics (for modulating the expression of  
 CC Akt-1), prophylaxis (e.g. to prevent or delay infection, inflammation,  
 CC or tumor formation), as research reagents (e.g. to distinguish between  
 CC members of a biological pathway) and in kits. The present sequence  
 CC represents the human Akt-1 DNA sequence (GenBank Accn number: M63167).  
 XX  
 SQ Sequence 2610 BP; 537 A; 752 C; 781 G; 540 T; 0 other:  
 Query Match 46.5%; Score 719.2; DB 20; Length 2610;  
 Best Local Similarity 70.3%; Pred. No. 7,1e-185;  
 Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;  
 QY 5 gtcataatgagcagatgttaccatgttgaagaagggttgggtcagaagaaggagagataat 64  
 DB 193 ggcacacatgagcagcgtgtgtatgttgaaggaggttgggtcagacaaagaggagagatc 252  
 QY 65 ataaaactgtgagcgcacagatctctcttgaagacagatgtgtcatcatagatatt 124  
 DB 253 atcaagacctgtgcgcgcacagcctactctcctcacaagaatgacgtcacttcatgtgtac 312  
 QY 125 aagaagaacccctcaagatgtgatttactta---tccctcaacaacttctcagtgca 181  
 DB 313 aagagagcgccgcagagatgtgtgacaaagctgtgaggtccctcaacaacttctcagtgca 372  
 QY 182 aaatgacagtttaataaagcagacacacacacacacacacacacacacacacacacacac 241  
 DB 373 cagtgcagctgtatgaaagcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 432  
 QY 242 cagtgcagctgtatgaaagcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 301  
 DB 433 cagtgcagcagctgtatgaaagcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 492  
 QY 302 tggacagagatcagcagcgtgtgacagacagcgtgcagagcagagagagagagagagag 361  
 DB 493 tggacagagcagcagcagcgtgtgacagacagcgtgcagagcagagagagagagagagag 552  
 QY 362 aatgttagtccactcaactcaaatatgataatagagagagagagagatgtatgtcctctaca 421  
 DB 553 gacttcggtcgtgcgtcaccacagcagcagcagcagcagcagcagcagcagcagcagcagc 612  
 QY 422 acccatc---ataaagaagaagaatgatttgcatttgaacttgaacttgaacttgaacttga 478  
 DB 613 gccaaagcccaagcagcagcgtgtgacacagcagcagcagcagcagcagcagcagcagcagc 672

QY	479	ggcacctttgggaaagtattttgtgtcagaggaagcgacagtggaataactatgctatg	538
Db	673	ggcaccttcggcaagtgatcccttgggtgaaaggaaaggccacagcgccgttactacgcctatg	732
QY	539	aagatcttggaaagaagaactcatatttgcgaaagaaatgaaatgtgcacacacttaactaa	598
Db	733	aagatcttcaagaagaagatcatctgtgcgcaaggaagatgtgtgcacacactacccag	792
QY	599	agcagagatattaagaacactatgacatcccttttaacatcccttgaataatctcttcag	658
Db	793	aaccgcgtccctgcagaactccacacccctccctccacacccctgaagatccttcacag	852
QY	659	acaaaagaccggtttgtttttttgttgggaatagttaatgtgggggcagatgtttttcat	718
Db	853	aaccacagaccgcctctgtcttgggttcacatggaatgaacgaacgggggcagatgtttcttcac	912
QY	719	ttgtcgaagagacgggtgttctctctcttgagagacggcacacgctttctatgtgtcagaataatc	778
Db	913	ctgtcccgaggaaacgtgtgtctctccgcaggaacggcgccgcttctatgtgcgttgatgttg	972
QY	779	tcgtcgttgactatctacatctccggaaga---ttgtgtacgggtgatctcaagtttgag	835
Db	973	tcagccctctgacttaccctgtccatctcggaagaagatgtgtgttaccgggacctccaagcttgag	1033
QY	836	aactaatgtctgacaaagaatgtgcacatataaataatcacagatttttgactttgcgaaga	895
Db	1033	aacctcatgtctgcagaagacgggcacacatlaagaatccacagacttcgggtctgcagaagag	1093
QY	896	ggagatcacagatgcagacacacatgaaagacatctgtgtgcactccagaatctctgcacaca	955
Db	1093	ggagatcaagaagcgtgtccacacatgaaagaccttttgggcacaccttgagtaactgtgcccc	1153
QY	956	gaggtgttgaagaagataatgtactatggccgagacgatacgtatgtgtggggtctagggttgtc	1015
Db	1153	gaaggctcgtgaaagacaatgtactacgcgcgtgtgcagatgactatgtgtggggtctggtgtctc	1212
QY	1016	atgcatataaatgatatgtgttgagaggtttaaccttctacaaacagacacatagaagaacttttt	1075
Db	1213	atgtaagcagatgatgtgtgcgtgtgcgcctctctacacacagagacacatagaagaacttttt	1272
QY	1076	gaatlaatatlaatgagagaacatlaaattctctcgacaacctctctcagatgcgaataatca	1133
Db	1273	gagctcatctctcatctgagagatctcgccttccgcgcagcgtgtgtcccgaggccaagtcc	1333
QY	1136	ttgtcttcacggcctctgataaaggatccaaataaagcgccttgggttgagagaccagatgat	1195
Db	1333	ttgtcttcacggcctcgcgcccaagaagagcccaacaaagagcttgcgtggggtctccgaagac	1393
QY	1196	gcaaaagaatatttgaagacacaaattcttctctcgtgagatlaaacatgbcgaagaatgatattat	1255
Db	1393	gccaagagatcatagacagatctgccttcttgcgcgfatcgtgttgagacagctgtacagag	1453
QY	1256	aaaaagcttgtaacctctctttaaacctcaagtaacatctgcagacagatactagatattt	1315
Db	1453	aagaagatctcagcccaaccttccaagccccaagtgatcagctcgagaaatgtaaccaagatattt	1513
QY	1316	gatbaagaatttcaagcttgagactatttaacataaacccgcctgaaanaatatgatagatg	1375
Db	1513	gatbaagaatttcaagggcccaagatcatcacatcaaccacactgtgacaa-----gatgac	1566
QY	1376	gtatgtaactgcagatgcagcaatgagagcgcgccgcatattccctcaatcttctactactgca	1435
Db	1567	agcatatgagtgtgtgtgagcagcgagcgagccccaacttccccaagtctctctacacgcgc	1626
QY	1436	agttgacgagaataatgc 1453	
Db	1627	agccagcacggccttgaggc 1644	

RESULT	13
AAA09076	
ID	AAA09076 standard; DNA; 2610 BP.

Accession	Gene	Location/Qualifiers
AA09076:		
XX	10-AUG-2000	(first entry)
XX	WT	Wild type human Akt coding sequence.
XX	DE	
XX	KW	Akt; protein kinase B; serine-threonine kinase; proto-oncogene; cardiant;
XX	RW	inhibitor; apoptosis; cell death; antiapoptotic; muscular active; ss.
XX	OS	
XX	OS	Homo sapiens.
XX	Key	Location/Qualifiers
XX	FT	199..1641
XX	FT	/tag= a
XX	FT	/product= protein_kinase_B
XX	FT	/note= "serine threonine kinase"
XX	PN	WO200020025-A2.
XX	PD	13-APR-2000.
XX	PF	29-SEP-1999; 99WO-US22633.
XX	PR	02-OCT-1998; 98US-0102740.
XX	PA	(SELI-) ST ELIZABETH'S MEDICAL CENT INC.
XX	PI	Walsh K;
XX	DR	WPI: 2000-303639/26.
XX	DR	P-PSDB; AAY92221.
XX	PT	Treating myocardial infarction or conditions associated with increased
XX	PT	apoptotic cell-death of vascular endothelial cells or skeletal
XX	PT	myocytes comprises administering Akt (also termed Protein Kinase B
XX	PT	(PKB)) molecule
XX	PS	Disclosure: Page 65-66; 71pp; English.
XX	CC	The invention concerns methods of treating myocardial infarction, which
XX	CC	comprise administering to a subject an Akt (Protein Kinase B) molecule
XX	CC	to inhibit cardiac tissue necrosis. Akt is a proto-oncogene which
XX	CC	encodes a serine threonine kinase. It inhibits apoptotic cell death, in
XX	CC	particular of cardiomyocytes, skeletal myocytes and/or vascular
XX	CC	endothelial cells. It is therefore also useful for treating muscular
XX	CC	dystrophy, spinal muscular atrophy, anabolic steroid-induced muscle
XX	CC	injury, skeletal muscle oxidative stress, physical exercise and
XX	CC	unloading-induced skeletal muscle atrophy. The Akt protein can also be
XX	CC	used in screening for an inhibitory agent that inhibits apoptotic
XX	CC	cell-death of cells.
XX	SO	Sequence 2610 BP; 537 A; 752 C; 781 G; 540 T; 0 other;
Query Match	46.5%;	Score 719.2; DB 21; Length 2610;
Best Local Similarity	70.3%;	Pred. No. 7.1e-185;
Matches 1025; Conservative	0;	Mismatches 418; Indels 15; Gaps 4;
Db	5	gtcatcatgagagatgttacccattgaaagaaggttggttcagaaagggagaatat 64
Db	193	ggacaccatgagagagatgtgtctatgttgagaagaggttgctgcgacaaacaggggagctac 252
Qy	65	ataaaacatgagagccaaagatactctcttttgaaagacagatggtctatcataagatat 124
Db	253	atcaagacctgagcgccacgcgtactctccccaagaatgatgacactcatgtgctac 312
Qy	125	aaaggaacacctcaagatggttactctta---tccccaacaaactttcaatggca 181
Db	313	aagggcgggccgcaagatggtgacaaacgttgaaggtcccccctcaaaactctctgtgcg 372
Qy	182	aatgccagttaatgaaacagaagacacaaagccaaacattatataatcagatgttc 241

Db	373	cagtcgcagctcgatgaaagacgagcgccgcgcgcgcacacacccctcatcatccgctgcctg	432
Qy	242	cagtcgactactgctatagagagaaacattctatgtatagatctccagaagagaaagagaa	301
Db	433	cagtcgacactgctatcccgaaacgcacccctccatgttgtagagctctcgagagcgcgagag	492
Qy	302	tggacaagaagctatctccagtcgtctgacgaacagactgcagagcgaaagaaagagagaaatg	361
Db	493	tggacaacagccatccacagactgtgtctgacgcgcctcaagaagacagagcgagagagatg	552
Qy	362	aattgtactccaactccaaattgataataatagggaaagaaagatgatatgtctcttaaca	421
Db	553	gaactccggtccgcgcctcaacccagctgacaactccagggcgctgaagaaagatgtgaggtccctg	612
Qy	422	accctac--aataaagaagaacacaatgaatgatttttaccatttggaaactactaggtaaa	478
Db	613	gccaaagccccaagacacgcggtgacccaatgaacgagttttgagtaacctggaagctgtctgcgaag	672
Qy	479	ggcactcttgagaaagtatttttggctcgagagaaagcgaaagtggaaataactatgctatg	538
Db	673	ggcactcttcgcgaaggtgatctcgttgaaagagagagccacagcgccgcctactaagcctatg	732
Qy	539	aagatctgaagaaagaaagatcatattatctgacaagagatgaaagtgcacacactactatgaa	598
Db	733	aagatccctcaagaagaaagatcatctgtgcacaagagacgaggttgcgccacacactacccag	792
Qy	599	agcagagatattaagaacacacatgacaccccttttaacatccctctggaatattccctccag	658
Db	793	aaccgcgtccctcgaaactccagacaccccttccctccacgcgccttgaaatgaactcttccag	852
Qy	659	acaaaagacggttctgtcttctgtgataatgtaataatgtatgtgggcagagctgtttccat	718
Db	853	accacacagccgcctctgtctgtcatgtagtaacgacaacggcgagctgtcttccac	912
Qy	719	ttgcgcgagagcgcggtgtctctcgcagagaccgcacacgctttctatgtgtcgaataatgttc	778
Db	913	ctgtccgcggagaaacgtgtgtctctccgaaagacacgcggccgcgcttctctatgtgcgttgaagtctg	972
Qy	779	tcgtgccttgagactctctacatctccgaaaga---ttgtgtacccgtatctcaagtgtgag	835
Db	973	tcagccctcgactacccgcacactcggagaaagaaacggtgtgtatccgggaacctcaagcttgag	1033
Qy	836	aattcatgcttgacaacaaagatgcccacataaaatactacagattttgagcttgcgaagaa	895
Db	1033	aactctatgcttgagacaagcgcgacatataagatcacagacttcggctgtgcgaagag	1092
Qy	896	ggagtcacagatgacgccacactagaagaatctctgtgacacctccacgaataatctgcgacca	955
Db	1093	ggagtcacagaaacggtgtgcacacatgaagaccttttgcgcacaccttgatgactctgtgcgcc	1152
Qy	956	gagatgtctaaagaagataatgactatggccgcgagcagatgactgtgtgggccttaagggtctc	1015
Db	1153	gaggtgcgtgagaaacaaatgactacgcgcgtgcagctgtagctgtgtggggtcgtgtgtgtc	1212
Qy	1016	atgtatgaaatgatatgtgtggaggttaaccttctactacaacagagacatgatgaaacctttt	1079
Db	1213	atgtatcagagatgtgtgtgcgtctgcgccttctactacaacagagacatgatgaaagctttt	1272
Qy	1076	gaatcatataatgaaagaaacataatttctcgcgaacactctcttcagatgacaaatca	1135
Db	1273	gagctactctctatgaaagagatccgcgtctcccgcgacgctgtgtcccgagccaaagctcc	1332
Qy	1136	ttgcttctcagagctctgtataaagaagatcccaataaacgcctctgtgtgcagagacaaatgt	1195
Db	1333	ttgcttctcagagctctgtatcaagaagagccccaagacagagctgtgcgggggtctccgagac	1392
Qy	1196	gcaaaagaaatattgagacaacagttctctctctctgtgagtaaacctgtgcgaagtatgat	1255
Db	1393	gccaagagagatcatgacagatcgtctcttgcgcggtatcgtgtgcagcaacgtgtgaag	1452
Qy	1256	aaaaagctgtactctctttaaactcaagaatgaatacttgaaacagataactagatattt	1315
Db	1453	aagaaagctacgcccacaccttcaagcccacaggttcaagctgtgaaagacagaaacaggtattt	1512

QY	1316	gatgaagaatttacaagctcagactattacaataacaccactgaaanaatgatgatgatg	1375
Db	1513	gattggggatttaccagccagatgatcatcatcacaccactgcacaa-----gatgac	1566
QY	1376	ggtatgagactctcatggaacaattgagaagcgcgccgcatlcttcctcaatttcttactctgca	1435
Db	1567	agcaatgagatgtgtgagacagcgagcgagcgcccaattcctcccaagtctctcactctggcc	1626
QY	1436	agtggacagagataatgc	1453
Db	1627	agcagcaacgagcttgagc	1644

## RESULT 14

AAV71037	
ID	AAV71037 standard; cDNA: 2181 BP.
XX	
AC	AAV71037;
XX	
DT	08-FEB-1999 (first entry)
XX	
DE	PKB-green fluorescent protein fusion product.
XX	
KW	Human: PKB gene; fusion protein; green fluorescent protein; GFP; intracellular signalling; chimera; ss.
OS	Chimeric - Aequorea victoria.
XX	
OS	Chimeric - Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
CD	1..2181
FT	/**tag= a
XX	
PN	WO9845704-A2.
PD	15-OCT-1998.
XX	
PE	07-APR-1998; 98WO-DK00145.
XX	
PR	07-APR-1997; 97DK-0000392.
XX	
PA	(NOVO ) NOVO-NORDISK AS.
PI	Kasper A, Petersen Bjorn S, Scudder K, Thastrup O; Tulin S;
DR	WP1: 1998-594491/50. P-PSDB; AAWB5022.
XX	
PT	Determining effect on signalling pathways in live cells from redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus, particularly for identifying toxins and potential therapeutic agents
XX	
PS	Claim 63; Pages 154-158; 326pp; English.
XX	
CC	The present sequence encodes a human PKB-green fluorescent protein fusion product. The fusion protein is used in an assay that exemplifies the invention. The specification describes how quantitative information about the influence of a molecule on a cellular response is obtained by recording the variation, caused by the molecule, on mechanically intact living cells, in the spatially distributed light emitted from a luminophore present in the cells. The variation in light emission is processed to provide information that correlates spatial distribution to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, and especially to screen for potentially affect intracellular signalling, to identify new drug targets.
XX	
Sequence	2181 BP; 500 A; 672 C; 644 G; 365 T; 0 other:



Query Match 46.3%; Score 716.4; DB 19; Length 2181;  
 Best Local Similarity 70.7%; Pred. No. 3.8e-184;  
 Matches 1015; Conservative 0; Mismatches 406; Indels 15; Gaps 4;

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OY 11 atgacgcatgttaccattgtgaagaaggctgggttcagaagaaggaggaatataataa
DB 1 atgagcgaagctgtctatgtgaagaaggctgtgcacaagaaggaggtacatacaag
OY 71 aactggagccagaactctctcttttgaagacagatggtctctatagaatataaagg
DB 61 accctggcgccagcagctactctctctcacaagaatgtgcacacttattgtccacaagg
OY 131 aaaccacaagatgtgattaccctta---tcccctcaaacctttccatggcaaatgc
DB 121 cggccgcaggaatgtgtgccaacggtgaaggctccctcaaaccttctctgtgcgcagtgc
OY 188 cagttatgaataaacaagacagcaccaaagccaaacattatataatcagatgtctcagttg
DB 181 cagctgatgaagcaggaagcggcccgcccaacactcatcctcgcgtcgcagtgc
OY 248 actactgttatagaagaacatttcatgtatgatactccagaagaaggaaagaatggaaca
DB 241 accactgtcatcgaacgcctctccatcgtgagactcctcgaaggagcggagagtgagaca
OY 308 gaagctatccagcgtctgaacagacagactgcagagcagaagaagagagaagaatgtatgt
DB 301 accgcacatccagactgtgtgtctgaagcctccaaagaagcaggaagagagatgtgaattc
OY 368 agtccaactccaacaattgaataatagagaagaagaatgagatgctctcaaacccat
DB 361 cggctcgggtctccaccagctgacacacacaggggctgagaagatgaggtgtccctgcgcaag
OY 428 c---ataaagaagaagaatgaatatttgaactatttgaactactagttaaggcact
DB 421 cccaagcagcggctgacccaatgaaagagcttgactcctgaagctcctcgtgcgaaggcact
OY 485 ttgggaaagttatttggctgcagagaagcgaagtggaaataactatctctgaagact
DB 481 ttccgcaaggtgatctcctgttgaagaagagccacagcgcgtactacgcctatgaagatc
OY 545 ctgaagaagaagatcattatttgcnaaagtgaaagtgcacacacttaactgaagcaga
DB 541 ctcaagaagaagatcaltcgtgcgaagcagaggtgcgccacacactcaccgagaacgcg
OY 605 gftaataagaacaactagacatcccttttaacatcccttgaatattcctccagacaataa
DB 601 gtccctgcagaactccaagcaccctctccacagcctgaagtaacttctccagaccac
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DB 661 gaccgctctcgtcttgcataatgagtaagcacaagggggagagctgttctccaccgtgcc
OY 725 agaagcgggtgtctctgaagaccgcaacagcttctatgtgagcagaatattctctgcc
DB 721 cgggaagcgtgttctcgcgaagaccggccgctctatagcgcggaagttgtgcagcc
OY 785 ttggaactctacattccggaaaga---tgtgtacgcgtgtactcctaagttgagaactca
DB 781 ctggactactctgactctggaagaacggtgtgtacgcggagactcaagttgagaacctc
OY 842 atgctggacaagaatgagcacaataaattttagaatttggacttgcgaagaaggagtc
DB 841 atgtctggacaagaatgagcacaataaattttagaacttgcggctgtgcagaaggagtc
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DB 901 aagagcgtgtgcacacatgaagaccttggcgccacacctgagtlactctgccccgaggtg
OY 962 ttagaagaataatgactatgagccgagcagatagactgtgtgggctcgtagggtgtcatgtat
DB 961 ctggaggaacaatgactatgagccgtgtcagltgagctgtgtgggctgtggcgtgtgtac
OY 1022 gaatgagtgtgtggaggttacccttctacaacccagacagacatgaagaacttttgaatta
  
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DB 1021 ggagatgagtgtggcgcctgtccctctacaaaccaggaacatgaagaacttttgaagtc
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DB 1141 tcaaggctgtctcaagaagaccccaagcagaggtctggcggggtctccaggaacgcgaag
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DB 1201 ggagatcatgcaacatgcctctcttccggtalacgtgtgacagacagtgtaagagaaga
OY 1262 ctgtgactcctctttaaacctaaatgaacatctgagacagatactagatatttgaatga
DB 1261 ctcaagccacccttcaagccccaggtcactgagatgagacacacaggtatttgaatgag
OY 1322 gaatttacagctcagactattacaataacacacacttgaaaatatgagatgtatg
DB 1321 gagttcaagcggccagatgtatcacatcacacacactgacaa-----gatgacagatg
OY 1382 gactgcattgacaatgagagcggcgacattccctcaaatcttctactctgcaag
DB 1375 gagtgtgtgtgacagagagcagcagcccccacttccccagttctctactcgcgcag

RESULT 15
AAT71252
ID AAT71252 standard; DNA; 1599 BP.
XX
AC AAT71252;
XX
DT 30-MAR-1998 (first entry)
XX
DE Mouse Akt-2 cognate transgene.
XX
KW Akt-2; cognate transgene; mouse; serine-threonine kinase; proto-oncogene;
KW cellular immunogen; cancer; self-determinant immunoreactivity; lymphoma;
KW cancer vaccination; breast carcinoma; colon carcinoma; immunotherapy; ss.
XX
OS Mus musculus.
XX
PN WO9725860-A1.
XX
PD 24-JUL-1997.
XX
PF 13-JAN-1997; 97WO-US00582..
XX
PR 19-JAN-1996; 96US-0010262.
XX
(PUVAL-) UNIV ALLEGHENY HEALTH SCI.
XX
PI England JM, Halpern MS.
XX
WP1: 1997-384993/35.
XX
DR Proto-oncogene immunogen - used in vaccine for the prevention and
XX treatment of cancer
XX
PS Disclosure: Page 55-56; 81pp; English.
XX
  
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This sequence represents the mouse Akt-2 cognate transgene (CTG).  
 CC Deletion of amino acids 148-234 of the encoded protein render the CTG  
 CC non-transforming. Akt-2 is a serine-threonine kinase. This sequence can  
 CC be used in the cellular immunogen of the invention. The cellular  
 CC immunogen of the invention is for immunising against the product of a  
 CC target proto-oncogene, over-expression of which is associated with  
 CC cancer, comprises host cells transfected with a construct containing at  
 CC least one transgene related to the proto-oncogene and driven by a strong  
 CC promoter. The product of the transgene induces immunoreactivity to host  
 CC self-determinants on the product of proto-oncogene. The cellular

CC Immunogens are used for protective vaccination against cancer (e.g.  
 CC carcinoma of breast or colon, or various lymphomas) and for immunotherapy  
 CC of cancer. Use of the immunogen eliminates the need to isolate  
 CC immunogenic, HLA host-matched peptides. The method is not based on immune  
 CC recognition of a determinant defined by a cancer-specific mutation and  
 CC generates a systemic (anti-metastatic) response.

SQ Sequence 1599 BP; 351 A; 487 C; 457 G; 304 T; 0 other;

Query Match 42.5%; Score 658.2; DB 18; Length 1599;  
 Best Local Similarity 67.7%; Pred. No. 1.9e-168;  
 Matches 988; Conservative 0; Mismatches 453; Indels 18; Gaps 4;

QY 5 gtcataatgagcgtttccattgtgaagaaggttggtttcagaagggagagatat 64  
 Db 82 gccacatgaaatgaggtgtctgtccatcaaaagaaggtgtccacaagcgtgtgataac 141  
 QY 65 ataaaaactgagagccaaagatacttccttttgaagacagatggtccatcatagatat 124  
 Db 142 atcaagacctggagcgcaacggttacttcctgtgaagaagcagcgctccctcatgtgtac 201  
 QY 125 aagaagaacctaaagatgtgttaaccttacc--tcaacaacttltcagtgtga 181  
 Db 202 aaggaagagcccgagccctgtatcagactctaccccttaacaacctctcgttagca 261  
 QY 182 aatgacgtttaaagaaacagacgaacaaagccaaacacatttaatactgattcc 241  
 Db 262 gaatgcacagctgtgagagagagagccgacccaaccttltcaltacgtgtcgt 321  
 QY 242 cagtgtactactgttataagagaacaatctcatgtatgatactcagaagaaagagaaga 301  
 Db 322 cagtgcacacagctatcgtgagagaccttccacgtgtgattctccagaagagagggag 381  
 QY 302 tgaacagaagcttccagctgtgacagagaagc-----gcagaagcagaagaagag 355  
 Db 382 tggatgcgggtccatcagatgtgtccaaacagctcaagcagcgccacagcgagagac 441  
 QY 356 agaatgaatgtatgtccaacttcacaatgtataatataagagaaggaagatgtgtcc 415  
 Db 442 cccatgtactacaaggtgtgtctcccaatgtactctccacagctgaagagaagtgagtg 501  
 QY 416 tctacaacccat---cataaaagaagaacaatgaatgtatgttgaactatttgaactacta 472  
 Db 502 gcggtcagcagaagcagcgggtlaaagtacacatgaatgtactcgaactatctcaactcctt 561  
 QY 473 ggtaaaggaacttttgggaagtatttgggtcgcagaagaagcagaatgtgaaatactat 532  
 Db 562 ggtcaagggaaaccttgtgcaaaagtcacccgtgtggtggaagagccactgtgcgtactac 621  
 QY 533 gctatgaagatctcgaagaagaagatcatatgtcacaagaagatgaagtgtgcacactcta 592  
 Db 622 gtcattgaagatctcgaagaagaagatcatatgtcacaagaagatgaagtgtgcacacagtc 681  
 QY 593 actgaagcagaatataaagaacactagaacatcccttttaacatccttgaatatcc 652  
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 QY 713 ttccattgtcgaagagcgggtgtctctcgaagaccgcacacgttttctatgtgtcagaa 772  
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 QY 773 atgtctgtccttgaactatcatlccggaagaatgtgtlacgtgtatctcaagtgtg 832  
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 QY 833 gagaatctaagtgtgacaagaatgtgcacataataataacagatttggactttgcaaa 892  
 Db 922 gaaaacctatgtgtgacaagaatgtgcacataacagatttggactttgcaaa 981

QY 893 gaaggatcacagatgtcacgaccatgaagaagacattctgtgtgcactccagatatctgtgca 952  
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 Db 1042 ccgaaggtgtgtgagaacaatgactatggccgagcagatgagctgtgtgtgtgtgtgtgtg 1101  
 QY 1013 gtcaatgtcaatgtatgt 1072  
 Db 1102 gtcatgtcaagatgtatgt 1161  
 QY 1073 ttggaatataatgaagaagaacatttaatttccctcgaagacactctctcgaatgtcaaaa 1132  
 Db 1162 ttcaagctatccctcgaagaagatgcgcgttcccgacagctcgaagcccgagggccaa 1221  
 QY 1133 tcaatgtctcaggggtctctgtatlaaagatcccaataaacgctctgtgtgagagaccagat 1192  
 Db 1222 tccctgtctgt 1281  
 QY 1193 gatgcagaagaatataatgagacacagttctctctctgtgtgtgtgtgtgtgtgtgtgt 1252  
 Db 1282 gatgcagaagaatataatgagacacagttctctctctgtgtgtgtgtgtgtgtgtgtgt 1341  
 QY 1253 gataaaagctgtgtactctctttaaactcaagtaacatctgagacagatactagatat 1312  
 Db 1342 cagaagaagctctctgtccaccttcaacctcaagtgatcgtccgaaggtgtgcacaaggtac 1401  
 QY 1313 ttgataagaagaattacaagctcagactatataacacacacactgtgaaataatgtagag 1372  
 Db 1402 ttgataatgaattatcagccagctccatcaatcaacacacacacacacacacacacacac 1455  
 QY 1373 gatgtatgactgtcagatgacaatgtgagagcgccgcatcttccatcaatttccactact 1432  
 Db 1456 gaagcctgt 1515  
 QY 1433 gcaagtgtgacagagaataag 1451  
 Db 1516 gccagatcgcgagtgag 1534

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Mon Mar 11 07:46:12 2002

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